

Supporting information

Figures

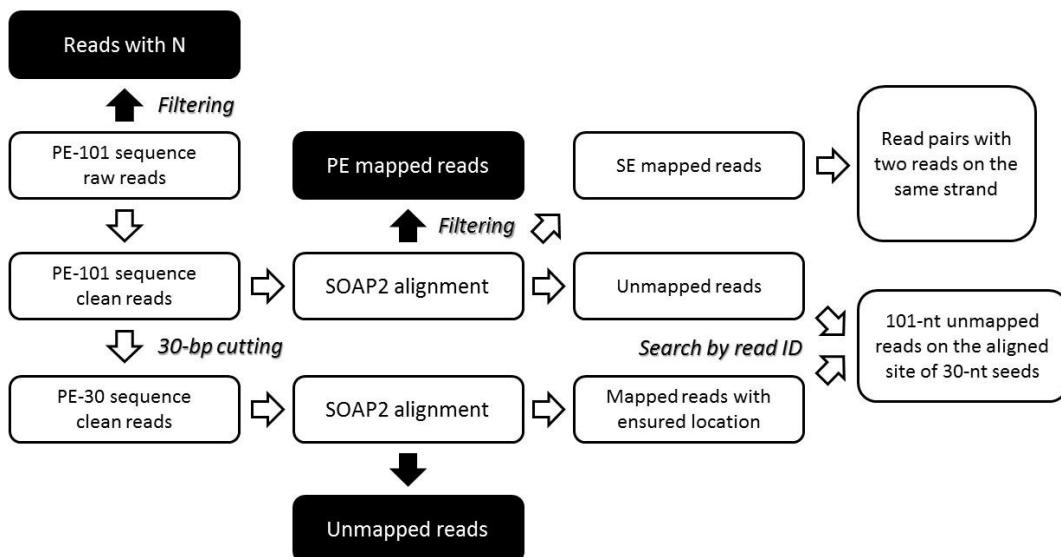


Figure A: Reads alignment and filtering

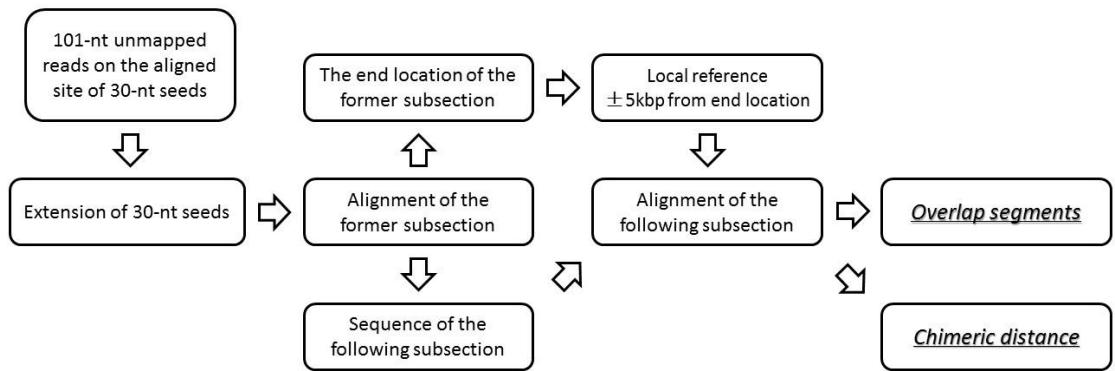


Figure B: Subsection alignment strategy used for the chimera discovery

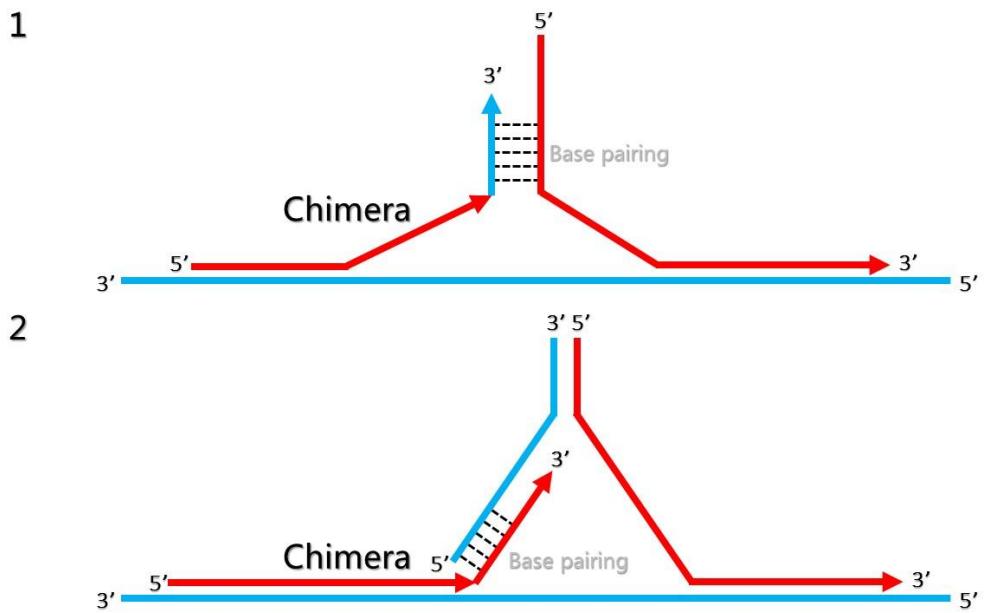


Figure C: The probable generating process of phi29 MDA chimeras based on the hyperbranched structure.

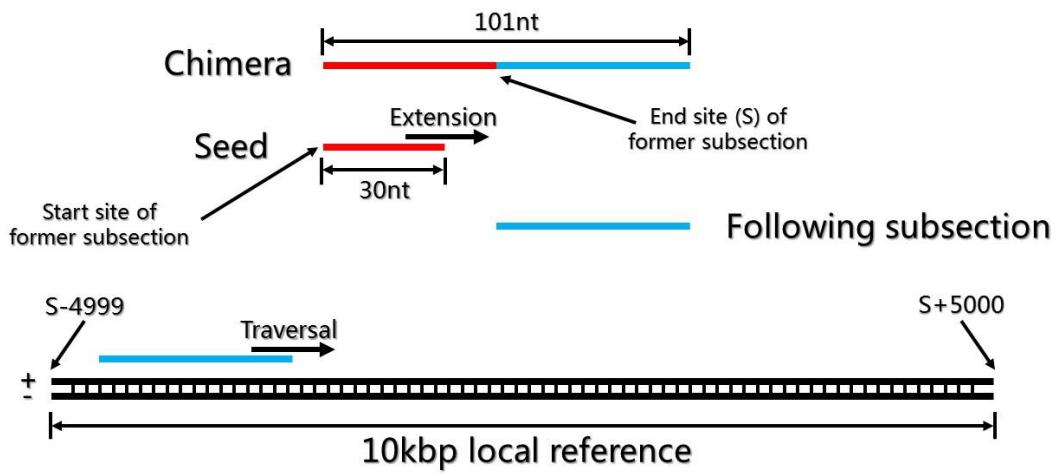


Figure D: Demonstration of the two core substeps (**seed extension** and **local alignment**) in the subsection alignment strategy.

Tables

Run number	Read pairs	Average insertion size	Insertion chimera	End chimera	Chimera ratio*
SRR799550	13371952	211.78	663962	213881	3.104
SRR799549	17068542	212.73	837201	269295	3.109
SRR799560	14184567	233.13	786364	232254	3.386
SRR799545	18297984	234.36	1021312	301806	3.384
SRR799547	14620324	237.41	1151644	337438	3.413
SRR799561	14456680	239.76	1106215	319198	3.466
SRR799558	17646526	240.47	1397000	404868	3.451
SRR799552	13365660	241.40	1108055	319539	3.468
SRR799546	15580764	241.72	917696	263291	3.485
SRR799553	16158737	242.00	945228	273189	3.460
SRR799559	18842904	242.45	1077455	311421	3.460
SRR799548	16156682	243.19	1337308	389258	3.436
SRR799556	16836834	243.31	973698	282962	3.441
SRR799557	15275461	243.52	1268411	365002	3.475
SRR799551	14445390	244.13	1234888	356872	3.460
SRR799544	14641175	244.46	870838	251165	3.467
SRR799554	13765673	244.70	1192499	342578	3.481
SRR799555	10802212	247.27	927978	264538	3.508

Table A: The data illustration of the 18 subsamples about the relationship between the average insertion size and the ratio of the insertion chimeras to the end chimeras

*Chimera ratio = Insertion chimeras / End chimeras